

Query= SEQ ID NO:1
(1509 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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Contig:AC119673.2.1.188119	<u>460</u>	e-126
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>Contig:AC119673.2.1.188119
Length = 188119

Score = 460 bits (232), Expect = e-126
Identities = 235/236 (99%)
Strand = Plus / Minus

Query: 255	agtcctttcctacagtgggtcagcaccagctttatccagcatgaagtcgtggaagagtatag	314
Sbjct: 172797	agtcctttcctacagtgggtcagcaccagctttatccagcatgaagtcgtggaagagtatag	172738

Query: 315	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	374
Sbjct: 172737	ccacctgttcactatccaaggctcggaccccagcttgcagccctacctgctgatggctca	172678

Query: 375	ctttgatgtggtgcctgcccctgaagaaggctgggaggtgccccattctctgggttgga	434
Sbjct: 172677	ctttgatgtggtgcctgcccctgaagaaggctgggaggtgccccattctctgggttgga	172618

Query: 435	gcgtgatggcgatcatctatgggtcggggcacactggacgacaagaactctgtgatgg	490
Sbjct: 172617	gcgtgatggcgatcatctatgggtcggggcacactggacgacaagaactctgtgatgg	172562

Score = 341 bits (172), Expect = 8e-91
Identities = 172/172 (100%)
Strand = Plus / Minus

Query: 1114	gaggtcctagaactcacgaagaacattgtggctgataacagagtccagttccatgtgttg	1173
Sbjct: 160007	gaggtcctagaactcacgaagaacattgtggctgataacagagtccagttccatgtgttg	159948

Query: 1174	agtgccctttgacccccctccccgtcagcccttctgatgacaaggccttgggctaccagctg	1233
Sbjct: 159947	agtgccctttgacccccctccccgtcagcccttctgatgacaaggccttgggctaccagctg	159888

Query: 1234	ctccgccagaccgtacagtccgtcttcccggaagtcaatattactgccccag	1285
Sbjct: 159887	ctccgccagaccgtacagtccgtcttcccggaagtcaatattactgccccag	159836

Score = 341 bits (172), Expect = 8e-91
Identities = 172/172 (100%)
Strand = Plus / Minus

Query: 1 atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct 60
|||||
Sbjct: 177310 atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct 177251

Query: 61 accgtctccagatcgatgggcccaggagcggggagcatcaaagggcgctcgcaatccct 120
|||||
Sbjct: 177250 accgtctccagatcgatgggcccaggagcggggagcatcaaagggcgctcgcaatccct 177191

Query: 121 tctcagttcagcaaagaggaacgcgtcgcgatgaaagaggcgctgaaagggtg 172
|||||
Sbjct: 177190 tctcagttcagcaaagaggaacgcgtcgcgatgaaagaggcgctgaaagggtg 177139

Score = 266 bits (134), Expect = 4e-68
Identities = 134/134 (100%)
Strand = Plus / Minus

Query: 575 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggctccagc 634
|||||
Sbjct: 171457 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggctccagc 171398

Query: 635 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 694
|||||
Sbjct: 171397 tagccttcattgtggacgaggggggcttcattcttgatgatttcattcctaacttcaaga 171338

Query: 695 agcccatcgcttg 708
|||||
Sbjct: 171337 agcccatcgcttg 171324

Score = 248 bits (125), Expect = 9e-63
Identities = 125/125 (100%)
Strand = Plus / Minus

Query: 1385 gcatccatggagtcaacgagaaaaatctcagtccaagcctatgagaccaagtgaattca 1444
|||||
Sbjct: 155447 gcatccatggagtcaacgagaaaaatctcagtccaagcctatgagaccaagtgaattca 155388

Query: 1445 tctttgagttgattcagaatgctgacacagaccaggagccagtttctcacctgcacaaac 1504
|||||
Sbjct: 155387 tctttgagttgattcagaatgctgacacagaccaggagccagtttctcacctgcacaaac 155328

Query: 1505 tgtga 1509
 |||||
Sbjct: 155327 tgtga 155323

Score = 238 bits (120), Expect = 8e-60
Identities = 120/120 (100%)
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacatgacttcagg 767
 |||||
Sbjct: 171024 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacatgacttcagg 170965

Query: 768 ccactcttcagctcctccaaaggagacaagcattggcatccttgcaagctgctgtcagccg 827
 |||||
Sbjct: 170964 ccactcttcagctcctccaaaggagacaagcattggcatccttgcaagctgctgtcagccg 170905

Score = 202 bits (102), Expect = 5e-49
Identities = 102/102 (100%)
Strand = Plus / Minus

Query: 1284 agttacttctattggcaacacagacagccgattctttacaaacctcaccactggcatcta 1343
 |||||
Sbjct: 157084 agttacttctattggcaacacagacagccgattctttacaaacctcaccactggcatcta 157025

Query: 1344 caggttctacccccatctacatacagcctgaagacttcaaacg 1385
 |||||
Sbjct: 157024 caggttctacccccatctacatacagcctgaagacttcaaacg 156983

Score = 178 bits (90), Expect = 7e-42
Identities = 93/94 (98%)
Strand = Plus / Minus

Query: 163 ctgaaagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 222
 |||||
Sbjct: 175216 ctgacagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 175157

Query: 223 gccctggctgagttcggaataacattcataaag 256
 |||||
Sbjct: 175156 gccctggctgagttcggaataacattcataaag 175123

Score = 174 bits (88), Expect = 1e-40
Identities = 88/88 (100%)
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 548
|||||
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 172077

Query: 549 cttcatttctctgggcatgatgaggag 576
|||||
Sbjct: 172076 cttcatttctctgggcatgatgaggag 172049

Score = 161 bits (81), Expect = 2e-36
Identities = 81/81 (100%)
Strand = Plus / Minus

Query: 964 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 1023
|||||
Sbjct: 169129 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 169070

Query: 1024 atattcaaagcaggggtcaag 1044
|||||
Sbjct: 169069 atattcaaagcaggggtcaag 169049

Score = 153 bits (77), Expect = 4e-34
Identities = 77/77 (100%)
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 886
|||||
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 169931

Query: 887 agcaactggcaaatgag 903
|||||
Sbjct: 169930 agcaactggcaaatgag 169914

Score = 151 bits (76), Expect = 2e-33
Identities = 76/76 (100%)
Strand = Plus / Minus

Query: 1043 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 1102
|||||
Sbjct: 167563 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 167504

Query: 1103 agacagtccaagaggt 1118
|||||||
Sbjct: 167503 agacagtccaagaggt 167488

Score = 131 bits (66), Expect = 1e-27
Identities = 66/66 (100%)
Strand = Plus / Minus

Query: 902 agtttcccttccctgtcaatataatcctgagcaacccatggctatttgaaccacttataa 961
|||||||
Sbjct: 169455 agtttcccttccctgtcaatataatcctgagcaacccatggctatttgaaccacttataa 169396

Query: 962 gcaggt 967
|||||
Sbjct: 169395 gcaggt 169390

Query= SEQ ID NO:3
(1086 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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Contig:AC119673.2.1.188119	<u>460</u>	e-127
----------------------------	------------	-------

>Contig:AC119673.2.1.188119
Length = 188119

Score = 460 bits (232), Expect = e-127
Identities = 235/236 (99%)
Strand = Plus / Minus

Query: 255	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgctggaagagtatag	314
Sbjct: 172797	agtctttcctacagtggtcagcaccagctttatccagcatgaagtcgctggaagagtatag	172738

Query: 315	ccacctgttcactatccaaggctcggaccccagcttgacgccctacctgctgatggctca	374
Sbjct: 172737	ccacctgttcactatccaaggctcggaccccagcttgacgccctacctgctgatggctca	172678

Query: 375	ctttgatgtggtgcctgccccctgaagaaggctgggaggtgccccattctctgggttga	434
Sbjct: 172677	ctttgatgtggtgcctgccccctgaagaaggctgggaggtgccccattctctgggttga	172618

Query: 435	gcgtgatggcgatcatctatggtcggggcacactggacgacaagaactctgtgatgg	490
Sbjct: 172617	gcgtgatggcgatcatctatggtcggggcacactggacgacaagaactctgtgatgg	172562

Score = 341 bits (172), Expect = 6e-91
Identities = 172/172 (100%)
Strand = Plus / Minus

Query: 1	atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct	60
Sbjct: 177310	atggctcagcgggtgcgtttgcgtgctggccctgggtggctatgctgctcctagttttccct	177251

Query: 61	accgtctccagatcgatgggccccgaggagcggggagcatcaaagggcgctcggaatccct	120
Sbjct: 177250	accgtctccagatcgatgggccccgaggagcggggagcatcaaagggcgctcggaatccct	177191

Query: 121	tctcagttcagcaaagaggaacgcgtcgcatgaaagaggcgctgaaagggtg	172
Sbjct: 177190	tctcagttcagcaaagaggaacgcgtcgcatgaaagaggcgctgaaagggtg	177139

Score = 266 bits (134), Expect = 3e-68
Identities = 134/134 (100%)
Strand = Plus / Minus

Query: 575 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 634
|||||
Sbjct: 171457 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaaggggcgtccagc 171398

Query: 635 tagccttcattgtggacgaggggggcttcattccttgatgatttcattcctaacttcaaga 694
|||||
Sbjct: 171397 tagccttcattgtggacgaggggggcttcattccttgatgatttcattcctaacttcaaga 171338

Query: 695 agcccatcgcccttg 708
|||||
Sbjct: 171337 agcccatcgcccttg 171324

Score = 238 bits (120), Expect = 6e-60
Identities = 120/120 (100%)
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 767
|||||
Sbjct: 171024 gattgcagtctcagagaaggggtccatgaacctcatgctgcaagtaaacaatgacttcagg 170965

Query: 768 ccactcttcagctcctccaaaggagacaagcattggcatccttgagctgctgtcagccg 827
|||||
Sbjct: 170964 ccactcttcagctcctccaaaggagacaagcattggcatccttgagctgctgtcagccg 170905

Score = 178 bits (90), Expect = 5e-42
Identities = 93/94 (98%)
Strand = Plus / Minus

Query: 163 ctgaaagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 222
|||||
Sbjct: 175216 ctgacagggtgcatccagattccaacagtgacttttagctctgagaagtccaataactaca 175157

Query: 223 gccctggctgagttcggaaaatacattcataaag 256
|||||
Sbjct: 175156 gccctggctgagttcggaaaatacattcataaag 175123

Score = 174 bits (88), Expect = 7e-41
Identities = 88/88 (100%)
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 548
|||||
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatcttt 172077

Query: 549 cttcatttctctgggccatgatgaggag 576
|||||
Sbjct: 172076 cttcatttctctgggccatgatgaggag 172049

Score = 161 bits (81), Expect = 1e-36
Identities = 81/81 (100%)
Strand = Plus / Minus

Query: 902 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 961
|||||
Sbjct: 169129 aggtttatggagagaaatcccttaaccaatgcaataatcaggaccaccacggcactcacc 169070

Query: 962 atattcaaagcaggggtcaag 982
|||||
Sbjct: 169069 atattcaaagcaggggtcaag 169049

Score = 157 bits (79), Expect = 2e-35
Identities = 79/79 (100%)
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 886
|||||
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttggaagcgggacagtgggtgactgtattgc 169931

Query: 887 agcaactggcaaatgaggt 905
|||||
Sbjct: 169930 agcaactggcaaatgaggt 169912

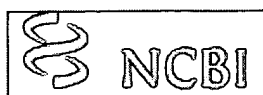
Score = 151 bits (76), Expect = 1e-33
Identities = 76/76 (100%)
Strand = Plus / Minus

Query: 981 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 1040
|||||
Sbjct: 167563 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 167504

Query: 1041 agacagtccaagaggt 1056
|||||
Sbjct: 167503 agacagtccaagaggt 167488

Score = 69.9 bits (35), Expect = 3e-09
Identities = 35/35 (100%)
Strand = Plus / Minus

Query: 1052 gaggtcctagaactcacgaagaacattgtggctga 1086
|||||
Sbjct: 160007 gaggtcctagaactcacgaagaacattgtggctga 159973



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Features

☐ 1: AC119673. Homo sapiens chro...[gi:34610310]

Links

LOCUS AC119673 187660 bp DNA linear PRI 13-SEP-2003
 DEFINITION Homo sapiens chromosome 1 clone RP11-212H11, complete sequence.
 ACCESSION AC119673 AL365208
 VERSION AC119673.3 GI:34610310
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 187660)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 187660)
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE 3 (bases 1 to 187660)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
 and Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE 4 (bases 1 to 187660)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 COMMENT On Sep 13, 2003 this sequence version replaced gi:21844627.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchtgs@u.washington.edu

Drafting Center: SC

----- Project Information

Center project name: chr-1

Center clone name: RP11-212H11 (sc0653)

----- Summary Statistics

Sequencing vector: unknown; 5% of reads

Sequencing vector: plasmid; 95% of reads

Chemistry: Dye-terminator ET; 43% of reads